

MAY 28 2002

19B
1MS
6-5-02

SEQUENCE LISTING

<110> Prayaga, Suhhirdas K
Shimkets, Richard A

<120> Novel Polypeptides and Polynucleotides Encoding Same

<130> 15966-615

<140> 09/782,436

<141> 2000-12-07

<150> 60/169,887

<151> 1999-12-09

<150> 60/170,230

<151> 1999-12-10

<160> 26

<170> PatentIn Ver. 2.1

<210> 1

<211> 475

<212> DNA

<213> Homo sapiens

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cagcctcttt ttacacaagg gcttgcttga tgcttggaat agggccttcc tggacaaact 180
ccagactgga tttcatcagc agctggaaga cctggagacc tgctttggta tagaggatgg 240
gaagcaagag tctgccctgg aaattgaggg ccctacactg gccataaaga ggtacttcca 300
gggagtacat ttcttcttga aagagaggaa attcaggaac tgtacctggg aggttgctcg 360
aatggtaaag ggatttttct taagcacaaa acttcaagaa aaagagaaca gaagaaaaga 420
gaactgcaaa aaaaatctgg aaaaggtaat ctatttagca gaagagtgaag agctg 475

<210> 2

<211> 154

<212> PRT

<213> Homo sapiens

<400> 2

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1 5 10 15
Ser Leu Phe Cys Asp Leu Pro Lys Ala Gln Val Ile Ser Ala Leu His
20 25 30
Lys Met His Gln Gln Ile Phe Ser Leu Phe Leu His Lys Gly Leu Ser
35 40 45
Asp Ala Trp Asn Arg Ala Phe Leu Asp Lys Leu Gln Thr Gly Phe His
50 55 60
Gln Gln Leu Glu Asp Leu Glu Thr Cys Phe Gly Ile Glu Asp Gly Lys

65 70 75 80

Gln Glu Ser Ala Leu Glu Ile Glu Gly Pro Thr Leu Ala Ile Lys Arg
85 90 95

Tyr Phe Gln Gly Val His Phe Phe Leu Lys Glu Arg Lys Phe Arg Asn
100 105 110

Cys Thr Trp Glu Val Val Val Met Val Lys Gly Phe Phe Leu Ser Thr
115 120 125

Lys Leu Gln Glu Lys Glu Asn Arg Arg Lys Glu Asn Cys Lys Lys Asn
130 135 140

Leu Glu Lys Val Ile Tyr Leu Ala Glu Glu
145 150

<210> 3
<211> 610
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (74)..(208)
<223> Wherein n is a or t or c or g.

<400> 3
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ctgcgacctg cctnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn 120
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn 180
nnnnnnnnnn nnnnnnnnnn nnnnnnnnaa agctcagggtg atttctgccc tccataagat 240
gcaccagcag atcttcagcc tctttttaca caagggcttg tctgatgctt ggaatagggc 300
cttcctggac aaactccaga ctggatttca tcagcagctg gaagacctgg agacctgctt 360
tggtatagag gatgggaagc aagagtctgc cctggaaatt gagggcccta cactggccat 420
aaagaggtag ttccaggagg tacattttctt cttgaaagag aggaaattca ggaactgtac 480
ctgggagggt gtcgtaatgg taaagggtt tttcttaagc acaaaacttc aagaaaaaga 540
gaacagaaga aaagagaact gcaaaaaaaa tctggaaaag gtaatctatt tagcagaaga 600
gtgaaagctg 610

<210> 4
<211> 199
<212> PRT
<213> Homo sapiens

<220>
<221> VARIANT
<222> (24)..(68)
<223> Wherein Xaa is any amino acid.

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1 5 10 15
Ser Leu Phe Cys Asp Leu Pro Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa

20					25					30									
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa					
35					40					45									
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa					
50					55					60									
Xaa	Xaa	Xaa	Xaa	Lys	Ala	Gln	Val	Ile	Ser	Ala	Leu	His	Lys	Met					
65					70					75					80				
Gln	Gln	Ile	Phe	Ser	Leu	Phe	Leu	His	Lys	Gly	Leu	Ser	Asp	Ala					
85					90					95									
Asn	Arg	Ala	Phe	Leu	Asp	Lys	Leu	Gln	Thr	Gly	Phe	His	Gln	Gln					
100					105					110									
Glu	Asp	Leu	Glu	Thr	Cys	Phe	Gly	Ile	Glu	Asp	Gly	Lys	Gln	Glu					
115					120					125									
Ala	Leu	Glu	Ile	Glu	Gly	Pro	Thr	Leu	Ala	Ile	Lys	Arg	Tyr	Phe					
130					135					140									
Gly	Val	His	Phe	Phe	Leu	Lys	Glu	Arg	Lys	Phe	Arg	Asn	Cys	Thr					
145					150					155					160				
Glu	Val	Val	Val	Met	Val	Lys	Gly	Phe	Phe	Leu	Ser	Thr	Lys	Leu					
165					170					175									
Glu	Lys	Glu	Asn	Arg	Arg	Lys	Glu	Asn	Cys	Lys	Lys	Asn	Leu	Glu					
180					185					190									
Val	Ile	Tyr	Leu	Ala	Glu	Glu													
195																			

<210> 5
 <211> 1887
 <212> DNA
 <213> Homo sapiens

<400> 5
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 ctaagcgtgc tgtgcccagg ggcaggcctc ctgttcgtgc caccctcgct ggaccgcccg 180
 gcagccgagc tgcggtggtc agacaacttc atcgccctcg tgcgcccgcg cgacctggcc 240
 aacatgacag gcctgctgca tctgagcctg tcgcggaaca ccatccgcca cgtggctgcc 300
 ggcgccttcg ccgacctgcg ggccttgcgt gccctgcacc tggatggcaa ccggctgacc 360
 tcactgggcg agggccagct gcgcggcctg gtcaacttgc gccacctcat cctcagcaac 420
 aaccagctgg cagcgctggc ggccggcgcc ctggatgatt gtgccgagac actggaggac 480
 ctcgacctct cctacaacaa cctcgagcag ctgccctggg aggccttggg ccgcctgggg 540
 aacgtcaaca cgttgggcct cgaccacaac ctgctggcct ctgtgcccgc cggcgctttt 600
 tccgcctgca acaagctggc ccggctggac atgacctcca accgcctgac cacaatccca 660
 cccgacccac tcttctcccc cctgccccctg ctgccaggc cccggggctc gcccgctct 720
 gccctggtgc tggcctttgg cgggaacccc ctgcactgca actgcgagct ggtgtggctg 780
 cgtcgcctgg cgcgggagga cgacctcgag gcctgcgcgt cccacactgc tctgggcggc 840
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cgctcaccac ctctggtgtgt gcccgcaggt cgcccggtgt ccttgcgtgt ccgggcagtg 960
ggggacccag agccccgtgt gcgttgggtg tcaccccagg gccggctgct aggcaactca 1020
agccgtgccc gcgccttccc caatgggacg ctggagctgc tggtcaccga gccgggtgat 1080
ggtggcatct tcacctgcat tgcggccaat gcagctggcg aggccacagc tgctgtggag 1140
ctgactgtgg gtccccacc acctcctcag ctagccaaca gcaccagctg tgaccccccg 1200
cgggacgggg atcctgatgc tctcacccca ccctccgctg cctctgcttc tgccaagggtg 1260
gccgacactg ggccccctac cgaccgtggc gtccagggtga ctgagcacgg ggccacagct 1320
gctcttgtcc agtggccgga tcagcggcct atccccgggca tccgcatgta ccagatccag 1380
tacaacagct cgggtgatga catcctcgtc tacaggatga tccccggcga gagccgctcg 1440
ttcctgctga cggacctggc gtcaggccgg acctacgata tgtgcgtgct cgccgtgtat 1500
gaggacagcg ccacgggggt cacggccacg cggcctgtgg gctgcgcccg cttctccacc 1560
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cgctacaagg tgcacggcgg ccagcccccc ggcaaggcca agattcccgc gcctgttagc 1740
agcgtttgct cccagaccaa cggcgccctg ggccccacgc ccacgcccgc cccgcccgcg 1800
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cccggccacg aacctgtggg accctag 1887

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<210> 6
<211> 628
<212> PRT
<213> Homo sapiens

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Ser Ser Pro Pro Gln Ser Ala Thr Pro Ser Pro Cys Pro Arg Arg Cys
      20              25              30

Arg Cys Gln Thr Gln Ser Leu Pro Leu Ser Val Leu Cys Pro Gly Ala
      35              40              45

Gly Leu Leu Phe Val Pro Pro Ser Leu Asp Arg Arg Ala Ala Glu Leu
  50              55              60

Arg Leu Ala Asp Asn Phe Ile Ala Ser Val Arg Arg Arg Asp Leu Ala
  65              70              75              80

Asn Met Thr Gly Leu Leu His Leu Ser Leu Ser Arg Asn Thr Ile Arg
      85              90              95

His Val Ala Ala Gly Ala Phe Ala Asp Leu Arg Ala Leu Arg Ala Leu
     100              105              110

His Leu Asp Gly Asn Arg Leu Thr Ser Leu Gly Glu Gly Gln Leu Arg
     115              120              125

Gly Leu Val Asn Leu Arg His Leu Ile Leu Ser Asn Asn Gln Leu Ala
     130              135              140

Ala Leu Ala Ala Gly Ala Leu Asp Asp Cys Ala Glu Thr Leu Glu Asp
     145              150              155              160

Leu Asp Leu Ser Tyr Asn Asn Leu Glu Gln Leu Pro Trp Glu Ala Leu
     165              170              175

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Gly Arg Leu Gly Asn Val Asn Thr Leu Gly Leu Asp His Asn Leu Leu
 180 185 190

Ala Ser Val Pro Ala Gly Ala Phe Ser Arg Leu His Lys Leu Ala Arg
 195 200 205

Leu Asp Met Thr Ser Asn Arg Leu Thr Thr Ile Pro Pro Asp Pro Leu
 210 215 220

Phe Ser Arg Leu Pro Leu Leu Ala Arg Pro Arg Gly Ser Pro Ala Ser
 225 230 235 240

Ala Leu Val Leu Ala Phe Gly Gly Asn Pro Leu His Cys Asn Cys Glu
 245 250 255

Leu Val Trp Leu Arg Arg Leu Ala Arg Glu Asp Asp Leu Glu Ala Cys
 260 265 270

Ala Ser Pro Pro Ala Leu Gly Gly Arg Tyr Phe Trp Ala Val Gly Glu
 275 280 285

Glu Glu Phe Val Cys Glu Pro Pro Val Val Thr His Arg Ser Pro Pro
 290 295 300

Leu Ala Val Pro Ala Gly Arg Pro Ala Ala Leu Arg Cys Arg Ala Val
 305 310 315 320

Gly Asp Pro Glu Pro Arg Val Arg Trp Val Ser Pro Gln Gly Arg Leu
 325 330 335

Leu Gly Asn Ser Ser Arg Ala Arg Ala Phe Pro Asn Gly Thr Leu Glu
 340 345 350

Leu Leu Val Thr Glu Pro Gly Asp Gly Gly Ile Phe Thr Cys Ile Ala
 355 360 365

Ala Asn Ala Ala Gly Glu Ala Thr Ala Ala Val Glu Leu Thr Val Gly
 370 375 380

Pro Pro Pro Pro Pro Gln Leu Ala Asn Ser Thr Ser Cys Asp Pro Pro
 385 390 395 400

Arg Asp Gly Asp Pro Asp Ala Leu Thr Pro Pro Ser Ala Ala Ser Ala
 405 410 415

Ser Ala Lys Val Ala Asp Thr Gly Pro Pro Thr Asp Arg Gly Val Gln
 420 425 430

Val Thr Glu His Gly Ala Thr Ala Ala Leu Val Gln Trp Pro Asp Gln
 435 440 445

Arg Pro Ile Pro Gly Ile Arg Met Tyr Gln Ile Gln Tyr Asn Ser Ser
 450 455 460

Ala Asp Asp Ile Leu Val Tyr Arg Met Ile Pro Ala Glu Ser Arg Ser
 465 470 475 480

Phe Leu Leu Thr Asp Leu Ala Ser Gly Arg Thr Tyr Asp Leu Cys Val
 485 490 495
 Leu Ala Val Tyr Glu Asp Ser Ala Thr Gly Leu Thr Ala Thr Arg Pro
 500 505 510
 Val Gly Cys Ala Arg Phe Ser Thr Glu Pro Ala Leu Arg Pro Cys Gly
 515 520 525
 Ala Pro His Ala Pro Phe Leu Gly Gly Thr Met Ile Ile Ala Leu Gly
 530 535 540
 Gly Val Ile Val Ala Ser Val Leu Val Phe Ile Phe Val Leu Leu Met
 545 550 555 560
 Arg Tyr Lys Val His Gly Gly Gln Pro Pro Gly Lys Ala Lys Ile Pro
 565 570 575
 Ala Pro Val Ser Ser Val Cys Ser Gln Thr Asn Gly Ala Leu Gly Pro
 580 585 590
 Thr Pro Thr Pro Ala Pro Pro Ala Pro Glu Pro Ala Ala Leu Arg Ala
 595 600 605
 His Thr Val Val Gln Leu Asp Cys Glu Pro Trp Gly Pro Gly His Glu
 610 615 620
 Pro Val Gly Pro
 625

<210> 7
 <211> 802
 <212> DNA
 <213> Equus caballus

<400> 7
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 ttttcccat ggccctcctg ccctctctct tgacggccct ggtggtgtac gagttatggc 180
 cctgtggagc tctgggctgt gacctgcctc agaaccacat cctgggttagc aggaagaact 240
 tcgtgcttct gggccaaatg agcagaatct cctccgcaat ctgtctgaag gacagaaaag 300
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 ctgtcctcca cgagatgctc cagcagatct tcagcctctt ccacacagag cgctcgtctg 420
 ctgcctggaa cagcaccctc ctggacgaac tctgcacggg actccttcgg cagctggaag 480
 acctggacac ctgtttggag caggagatgg gagaggaaga atctgccctg ggaactgtgc 540
 gccctacact ggccgtgaag aggtacttcc gggggatcca tctctacctg aaagagaaga 600
 aatacagtga ctgtgcctgg gagattgtcc gaatggaaat catgagatcc ttctcttcat 660
 cagcaaacct gcaaggaagg ttaagaatga aggatggaga cctgggctca ccttgaaatg 720
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 tcttatttct gctttagtct ag 802

<210> 8
 <211> 195
 <212> PRT

<213> Homo sapiens

<400> 8

Met Ala Leu Leu Phe Pro Leu Leu Ala Ala Leu Val Met Thr Ser Tyr
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Ser Pro Val Gly Ser Leu Gly Cys Asp Leu Pro Gln Asn His Gly Leu
20 25 30

Leu Ser Arg Asn Thr Leu Val Leu Leu His Gln Met Arg Arg Ile Ser
35 40 45

Pro Phe Leu Cys Leu Lys Asp Arg Arg Asp Phe Arg Phe Pro Gln Glu
50 55 60

Met Val Lys Gly Ser Gln Leu Gln Lys Ala His Val Met Ser Val Leu
65 70 75 80

His Glu Met Leu Gln Gln Ile Phe Ser Leu Phe His Thr Glu Arg Ser
85 90 95

Ser Ala Ala Trp Asn Met Thr Leu Leu Asp Gln Leu His Thr Gly Leu
100 105 110

His Gln Gln Leu Gln His Leu Glu Thr Cys Leu Leu Gln Val Val Gly
115 120 125

Glu Gly Glu Ser Ala Gly Ala Ile Ser Ser Pro Ala Leu Thr Leu Arg
130 135 140

Arg Tyr Phe Gln Gly Ile Arg Val Tyr Leu Lys Glu Lys Lys Tyr Ser
145 150 155 160

Asp Cys Ala Trp Glu Val Val Arg Met Glu Ile Met Lys Ser Leu Phe
165 170 175

Leu Ser Thr Asn Met Gln Glu Arg Leu Arg Ser Lys Asp Arg Asp Leu
180 185 190

Gly Ser Ser
195

<210> 9

<211> 195

<212> PRT

<213> Equus caballus

<400> 9

Met Ala Phe Ser Val Ser Ser Leu Met Ala Leu Val Val Ile Ser Ser
1 5 10 15

Ser Pro Val Ser Ser Met Ser Cys Asp Leu Pro Ala Ser Leu Asp Leu
20 25 30

Arg Lys Gln Glu Thr Leu Arg Val Leu His Gln Met Glu Thr Ile Ser
35 40 45

Pro Pro Ser Cys Leu Lys His Arg Thr Asp Phe Arg Phe Pro Gln Glu
 50 55 60
 Gln Leu Asp Gly Arg Gln Phe Pro Glu Ala Gln Ala Thr Ser Val Leu
 65 70 75 80
 Gln Glu Met Leu Gln Gln Ile Val Ser Leu Phe His Thr Glu Arg Ser
 85 90 95
 Ser Ala Ala Trp Asn Thr Thr Leu Leu Asp Arg Leu Leu Ala Gly Leu
 100 105 110
 His Gln Gln Leu Glu Asp Leu Asn Thr Cys Leu Asp Glu Gln Thr Gly
 115 120 125
 Glu Glu Glu Ser Ala Leu Gly Thr Val Gly Pro Thr Leu Ala Val Lys
 130 135 140
 Arg Tyr Phe Arg Arg Ile Arg Leu Tyr Leu Thr Glu Lys Lys Tyr Ser
 145 150 155 160
 Asp Cys Ala Trp Glu Ile Val Arg Val Asp Ile Met Arg Ser Phe Ser
 165 170 175
 Ser Ser Ala Asn Leu Gln Gly Arg Leu Gly Met Lys Asp Gly Asp Leu
 180 185 190
 Gly Ser Pro
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<210> 10
 <211> 117
 <212> PRT
 <213> Artificial Sequence

<220>
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 Domain 71-187

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 Ile Phe His Phe Phe Cys Thr Glu Ala Ser Ser Ser Ala Ala Trp Asn
 20 25 30
 Thr Thr Leu Leu Glu Glu Phe Cys Thr Gly Leu Asp Arg Gln Leu Thr
 35 40 45
 Arg Leu Glu Ala Cys Val Leu Gln Glu Val Glu Glu Gly Glu Ala Pro
 50 55 60
 Leu Thr Asn Glu Asp Ile His Pro Glu Asp Ser Ile Leu Arg Asn Tyr
 65 70 75 80

Phe Gln Arg Leu Ser Leu Tyr Leu Gln Glu Lys Lys Tyr Ser Pro Cys
85 90 95

Ala Trp Glu Ile Val Arg Ala Glu Ile Met Arg Ser Leu Tyr Tyr Ser
100 105 110

Ser Thr Ala Leu Gln
115

<210> 11
<211> 194
<212> PRT
<213> Felis catus

<400> 11
Met Ala Leu Pro Ser Ser Phe Leu Val Ala Leu Val Ala Leu Gly Cys
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Asn Ser Val Cys Ser Leu Gly Cys Asp Leu Pro Gln Thr His Gly Leu
20 25 30

Leu Asn Arg Arg Ala Leu Thr Leu Leu Gly Gln Met Arg Arg Leu Pro
35 40 45

Ala Ser Ser Cys Gln Lys Asp Arg Asn Asp Phe Ala Phe Pro Gln Asp
50 55 60

Val Phe Gly Gly Asp Gln Ser His Lys Ala Gln Ala Leu Ser Val Val
65 70 75 80

His Val Thr Asn Gln Lys Ile Phe His Phe Phe Cys Thr Glu Ala Ser
85 90 95

Ser Ser Ala Ala Trp Asn Thr Thr Leu Leu Glu Glu Phe Cys Thr Gly
100 105 110

Leu Asp Arg Gln Leu Thr Arg Leu Glu Ala Cys Val Leu Gln Glu Val
115 120 125

Glu Glu Gly Glu Ala Pro Leu Thr Asn Glu Asp Ile His Pro Glu Asp
130 135 140

Ser Ile Leu Arg Asn Tyr Phe Gln Arg Leu Ser Leu Tyr Leu Gln Glu
145 150 155 160

Lys Lys Tyr Ser Pro Cys Ala Trp Glu Ile Val Arg Ala Glu Ile Met
165 170 175

Arg Ser Leu Tyr Tyr Ser Ser Thr Ala Leu Gln Lys Arg Leu Arg Ser
180 185 190

Glu Lys

<210> 12

<211> 195
 <212> PRT
 <213> Homo sapiens

<400> 12

Met	Ala	Phe	Val	Leu	Ser	Leu	Leu	Met	Ala	Leu	Val	Leu	Val	Ser	Tyr
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		20						25					30		
Val	Gly	Arg	Lys	Asn	Leu	Arg	Leu	Leu	Asp	Glu	Met	Arg	Arg	Leu	Ser
		35					40					45			
Pro	His	Phe	Cys	Leu	Gln	Asp	Arg	Lys	Asp	Phe	Ala	Leu	Pro	Gln	Glu
	50					55					60				
Met	Val	Glu	Gly	Gly	Gln	Leu	Gln	Glu	Ala	Gln	Ala	Ile	Ser	Val	Leu
65					70					75					80
His	Glu	Met	Leu	Gln	Gln	Ser	Phe	Asn	Leu	Phe	His	Thr	Glu	His	Ser
				85					90					95	
Ser	Ala	Ala	Trp	Asp	Thr	Thr	Leu	Leu	Glu	Pro	Cys	Arg	Thr	Gly	Leu
			100					105					110		
His	Gln	Gln	Leu	Asp	Asn	Leu	Asp	Ala	Cys	Leu	Gly	Gln	Val	Met	Gly
		115					120					125			
Glu	Glu	Asp	Ser	Ala	Leu	Gly	Arg	Thr	Gly	Pro	Thr	Leu	Ala	Leu	Lys
	130					135					140				
Arg	Tyr	Phe	Gln	Gly	Ile	His	Val	Tyr	Leu	Lys	Glu	Lys	Gly	Tyr	Ser
145					150					155					160
Asp	Cys	Ala	Trp	Glu	Thr	Val	Arg	Leu	Glu	Ile	Met	Arg	Ser	Phe	Ser
			165						170					175	
Ser	Leu	Ile	Ser	Leu	Gln	Glu	Arg	Leu	Arg	Met	Met	Asp	Gly	Asp	Leu
		180						185					190		
Ser	Ser	Pro													
		195													

<210> 13
 <211> 195
 <212> PRT
 <213> Equus caballus

<400> 13

Met	Ala	Leu	Leu	Pro	Ser	Leu	Leu	Thr	Ala	Leu	Val	Val	Tyr	Glu	Leu
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Trp	Pro	Cys	Gly	Ala	Leu	Gly	Cys	Asp	Leu	Pro	Gln	Asn	His	Ile	Leu
			20					25					30		

Val Ser Arg Lys Asn Phe Val Leu Leu Gly Gln Met Ser Arg Ile Ser
 35 40 45
 Ser Ala Ile Cys Leu Lys Asp Arg Lys Asp Phe Arg Phe Pro Gln Asp
 50 55 60
 Met Ala Asp Gly Arg Gln Phe Pro Glu Ala Gln Ala Ala Ser Val Leu
 65 70 75 80
 His Glu Met Leu Gln Gln Ile Phe Ser Leu Phe His Thr Glu Arg Ser
 85 90 95
 Ser Ala Ala Trp Asn Thr Thr Leu Leu Asp Glu Leu Cys Thr Gly Leu
 100 105 110
 Leu Arg Gln Leu Glu Asp Leu Asp Thr Cys Leu Glu Gln Glu Met Gly
 115 120 125
 Glu Glu Glu Ser Ala Leu Gly Thr Val Arg Pro Thr Leu Ala Val Lys
 130 135 140
 Arg Tyr Phe Arg Gly Ile His Leu Tyr Leu Lys Glu Lys Lys Tyr Ser
 145 150 155 160
 Asp Cys Ala Trp Glu Ile Val Arg Met Glu Ile Met Arg Ser Phe Ser
 165 170 175
 Ser Ser Ala Asn Leu Gln Gly Arg Leu Arg Met Lys Asp Gly Asp Leu
 180 185 190
 Gly Ser Pro
 195

<210> 14
 <211> 195
 <212> PRT
 <213> Homo sapiens

<400> 14
 Met Ala Leu Leu Phe Pro Leu Leu Ala Ala Leu Val Met Thr Ser Tyr
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 Ser Pro Val Gly Ser Leu Gly Cys Asp Leu Pro Gln Asn His Gly Leu
 20 25 30
 Leu Ser Arg Asn Thr Leu Val Leu Leu His Gln Met Arg Arg Ile Ser
 35 40 45
 Pro Phe Leu Cys Leu Lys Asp Arg Arg Asp Phe Arg Phe Pro Gln Glu
 50 55 60
 Met Val Lys Gly Ser Gln Leu Gln Lys Ala His Val Met Ser Val Leu
 65 70 75 80
 His Glu Met Leu Gln Gln Ile Phe Ser Leu Phe His Thr Glu Arg Ser
 85 90 95

Ser Ala Ala Trp Asn Met Thr Leu Leu Asp Gln Leu His Thr Gly Leu
 100 105 110
 His Gln Gln Leu Gln His Leu Glu Thr Cys Leu Leu Gln Val Val Gly
 115 120 125
 Glu Gly Glu Ser Ala Gly Ala Ile Ser Ser Pro Ala Leu Thr Leu Arg
 130 135 140
 Arg Tyr Phe Gln Gly Ile Arg Val Tyr Leu Lys Glu Lys Lys Tyr Ser
 145 150 155 160
 Asp Cys Ala Trp Glu Val Val Arg Met Glu Ile Met Lys Ser Leu Phe
 165 170 175
 Leu Ser Thr Asn Met Gln Glu Arg Leu Arg Ser Lys Asp Arg Asp Leu
 180 185 190
 Gly Ser Ser
 195

<210> 15
 <211> 65
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:Consensus
 sequence

<400> 15
 Ala Gln Ser Val Leu His Met Gln Gln Ile Phe Leu Phe Thr Glu Ser
 1 5 10 15
 Ser Ala Ala Trp Asn Thr Leu Leu Thr Gly Leu Gln Leu Leu Cys Gln
 20 25 30
 Gly Glu Glu Ser Ala Leu Pro Leu Arg Tyr Phe Gln Gly Tyr Leu Lys
 35 40 45
 Glu Lys Lys Tyr Ser Cys Ala Trp Glu Val Arg Glu Ile Met Ser Leu
 50 55 60
 Gln
 65

<210> 16
 <211> 166
 <212> PRT
 <213> Homo sapiens

<400> 16
 Met Ser Tyr Asn Leu Leu Gly Phe Leu Gln Arg Ser Ser Asn Phe Gln
 1 5 10 15

Cys Gln Lys Leu Leu Trp Gln Leu Asn Gly Arg Leu Glu Tyr Cys Leu
 20 25 30
 Lys Asp Arg Met Asn Phe Asp Ile Pro Glu Glu Ile Lys Gln Leu Gln
 35 40 45
 Gln Phe Gln Lys Glu Asp Ala Ala Leu Thr Ile Tyr Glu Met Leu Gln
 50 55 60
 Asn Ile Phe Ala Ile Phe Arg Gln Asp Ser Ser Ser Thr Gly Trp Asn
 65 70 75 80
 Glu Thr Ile Val Glu Asn Leu Leu Ala Asn Val Tyr His Gln Ile Asn
 85 90 95
 His Leu Lys Thr Val Leu Glu Glu Lys Leu Glu Lys Glu Asp Phe Thr
 100 105 110
 Arg Gly Lys Leu Met Ser Ser Leu His Leu Lys Arg Tyr Tyr Gly Arg
 115 120 125
 Ile Leu His Tyr Leu Lys Ala Lys Glu Tyr Ser His Cys Ala Trp Thr
 130 135 140
 Ile Val Arg Val Glu Ile Leu Arg Asn Phe Tyr Phe Ile Asn Arg Leu
 145 150 155 160
 Thr Gly Tyr Leu Arg Asn
 165

<210> 17
 <211> 165
 <212> PRT
 <213> Homo sapiens

<400> 17
 Cys Asp Leu Pro Gln Thr His Ser Leu Gly Ser Arg Arg Thr Leu Met
 1 5 10 15
 Leu Leu Ala Gln Met Arg Arg Ile Ser Leu Phe Ser Cys Leu Lys Asp
 20 25 30
 Arg His Asp Phe Gly Phe Pro Gln Glu Glu Phe Gly Asn Gln Phe Gln
 35 40 45
 Lys Ala Glu Thr Ile Pro Val Leu His Glu Met Ile Gln Gln Ile Phe
 50 55 60
 Asn Leu Phe Ser Thr Lys Asp Ser Ser Ala Ala Trp Asp Glu Thr Leu
 65 70 75 80
 Leu Asp Lys Phe Tyr Thr Glu Leu Tyr Gln Gln Leu Asn Asp Leu Glu
 85 90 95
 Ala Cys Val Ile Gln Gly Val Gly Val Thr Glu Thr Pro Leu Met Asn

100	105	110
Glu Asp Ser Ile Leu Ala Val Arg Lys Tyr Phe Gln Arg Ile Thr Leu		
115	120	125
Tyr Leu Lys Glu Lys Lys Tyr Ser Pro Cys Ala Trp Glu Val Val Arg		
130	135	140
Ala Glu Ile Met Arg Ser Phe Ser Leu Ser Thr Asn Leu Gln Glu Ser		
145	150	155
Leu Arg Ser Lys Glu		
165		

<210> 18
 <211> 189
 <212> PRT
 <213> Mus musculus

<400> 18
Met Ala Arg Leu Cys Ala Phe Leu Met Val Leu Ala Val Met Ser Tyr
1 5 10 15
Trp Pro Thr Cys Ser Leu Gly Cys Asp Leu Pro Gln Thr His Asn Leu
20 25 30
Arg Asn Lys Arg Ala Leu Thr Leu Leu Val Gln Met Arg Arg Leu Ser
35 40 45
Pro Leu Ser Cys Leu Lys Asp Arg Lys Asp Phe Gly Phe Pro Gln Glu
50 55 60
Lys Val Asp Ala Gln Gln Ile Lys Lys Ala Gln Ala Ile Pro Val Leu
65 70 75 80
Ser Glu Leu Thr Gln Gln Ile Leu Asn Ile Phe Thr Ser Lys Asp Ser
85 90 95
Ser Ala Ala Trp Asn Ala Thr Leu Leu Asp Ser Phe Cys Asn Asp Leu
100 105 110
His Gln Gln Leu Asn Asp Leu Gln Gly Cys Leu Met Gln Gln Val Gly
115 120 125
Val Gln Glu Phe Pro Leu Thr Gln Glu Asp Ala Leu Leu Ala Val Arg
130 135 140
Lys Tyr Phe His Arg Ile Thr Val Tyr Leu Arg Glu Lys Lys His Ser
145 150 155 160
Pro Cys Ala Trp Glu Val Val Arg Ala Glu Val Trp Arg Ala Leu Ser
165 170 175
Ser Ser Ala Asn Val Leu Gly Arg Leu Arg Glu Glu Lys
180 185

<210> 19
 <211> 195
 <212> PRT
 <213> Antilocapra americana

<400> 19
 Met Ala Gln Leu Leu Pro Leu Leu Thr Ala Leu Val Leu Cys Ser Tyr
 1 5 10 15
 Gly Pro Val Gly Ser Leu Gly Cys Asp Leu Pro His Asn Ser Ala Pro
 20 25 30
 Leu Ser Arg Lys Thr Leu Val Leu Leu Asp Gln Met Arg Arg Val Ser
 35 40 45
 Pro Val Leu Cys Leu Lys Asp Arg Arg Asp Phe Gln Phe Pro Arg Glu
 50 55 60
 Val Val Asn Gly Ser Gln Phe Gln Lys Asn Gln Thr Val Ser Val Leu
 65 70 75 80
 His Glu Met Leu Gln Gln Ile Phe Asn Leu Leu His Thr Ala Arg Ser
 85 90 95
 Ser Ala Ala Trp Asn Asn Thr Leu Leu Glu Glu Leu His Thr Ala Leu
 100 105 110
 His Gln Gln Leu Gln Gly Leu Glu Thr Cys Leu Val Gln Ala Met Gly
 115 120 125
 Glu Glu Asp Ser Val Leu Thr Ala Asp Ser Pro Met Leu Met Leu Lys
 130 135 140
 Arg Tyr Phe Gln Arg Ile Arg Leu Tyr Leu Asp Glu Lys Lys His Ser
 145 150 155 160
 Gly Cys Ala Trp Glu Leu Val Arg Met Glu Ile Arg Arg Ala Phe Ser
 165 170 175
 Ser Thr Ala Asp Leu Gln Glu Ser Leu Arg Ser Lys Asp Gly Asp Leu
 180 185 190
 Ala Ser Ser
 195

<210> 20
 <211> 43
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:Consensus
 sequence

<400> 20

Phe Pro Glu Gln Lys Leu Glu Met Gln Gln Ile Phe Phe Ser Ser Ala
 1 5 10 15

Trp Asn Thr Leu Gln Gln Leu Leu Cys Gly Leu Leu Tyr Phe Arg Ile
 20 25 30

Tyr Leu Glu Lys Lys Ser Cys Ala Trp Glu Val
 35 40

<210> 21

<211> 184

<212> PRT

<213> Equus caballus

<400> 21

Met Ala Leu Pro Val Ser Leu Leu Met Ala Leu Val Val Leu Ser Cys
 1 5 10 15

His Ser Ile Cys Ser Leu Gly Cys Asp Leu Pro His Thr His Ser Leu
 20 25 30

Gly Asn Thr Arg Val Leu Met Leu Leu Gly Gln Met Arg Arg Ile Ser
 35 40 45

Pro Phe Ser Cys Leu Lys Asp Arg Asn Asp Phe Gly Phe Pro Gln Glu
 50 55 60

Val Phe Asp Gly Asn Gln Phe Arg Lys Pro Gln Ala Ile Ser Ala Val
 65 70 75 80

His Glu Thr Ile Gln Gln Ile Phe His Leu Phe Ser Thr Asp Gly Ser
 85 90 95

Ser Ala Ala Trp Asp Glu Ser Leu Leu Asp Lys Leu Tyr Thr Gly Leu
 100 105 110

Tyr Gln Gln Leu Thr Glu Leu Glu Ala Cys Leu Ser Gln Glu Val Gly
 115 120 125

Val Glu Glu Thr Pro Leu Met Asn Glu Asp Ser Leu Leu Ala Val Arg
 130 135 140

Arg Tyr Phe Gln Arg Ile Ala Leu Tyr Leu Gln Glu Lys Lys Tyr Ser
 145 150 155 160

Pro Cys Ala Trp Glu Ile Val Arg Ala Glu Ile Met Arg Ser Phe Ser
 165 170 175

Ser Ser Thr Asn Leu Pro Gln Ser
 180

<210> 22

<211> 92

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Consensus
sequence

<400> 22

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Ser Leu Leu Ala Leu Val Ser Leu Gly Cys Asp Leu Pro His Leu Leu
  1               5               10               15

Leu Gln Met Arg Cys Lys Asp Arg Asp Phe Phe Pro Gln Gly Gln Lys
      20               25               30

Ala Gln Ser His Gln Gln Ile Phe Leu Phe Thr Ser Ser Ala Ala Trp
      35               40               45

Asn Leu Leu Asp Leu Thr Gly Leu Gln Leu Leu Glu Cys Gln Glu Gly
      50               55               60

Glu Leu Leu Arg Tyr Phe Gln Tyr Leu Glu Lys Lys Tyr Ser Cys Ala
      65               70               75               80

Trp Glu Val Arg Glu Ile Met Ser Ser Thr Leu Gln
      85               90
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<210> 23

<211> 3144

<212> DNA

<213> Homo sapiens

<400> 23

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tcttcgatcc ggaaaatcct accggcatcc tcctaggagg ggattattat tattattttt 180
ctttaatctg gaagagaaga gaacaagttg tgcttttccc cccttcttct tgctaaacgc 240
catggatata actgaataag cggtcagggg ctttccccgc gtggacgtcc gaggccacca 300
tctgcctgca ttgcgcggag ccgcgcggag gtttagctcg agtctgtctc gggcggggaa 360
ggatgcgtgg ccgagccggg gagcccgggc gccccgcgga gccggcctcg gtgccaccca 420
gccgggggta gatgctgcct cggccaggcg ctgagtgacc agaccatgga gaccctgctt 480
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cacatcagcc gccaggactt tgccaacatg acggggctgg tggacctgac cctgtccagg 720
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gatgaccgcc tggtagggaa ctctcaagg accgctgtct atgacaatgg caccctggac 1500
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gcaagcggct ttggattgct tatg 3144

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<210> 24

<211> 832

<212> PRT

<213> Homo sapiens

<400> 24

Leu Glu Ser Val Ser Gly Gly Glu Gly Cys Val Ala Glu Pro Gly Ser
1 5 10 15

Pro Gly Ala Pro Arg Ser Arg Pro Arg Cys His Pro Ala Gly Gly Arg
20 25 30

Cys Cys Leu Ala Gln Ala Leu Ser Asp Gln Thr Met Glu Thr Leu Leu
35 40 45

Gly Gly Leu Leu Ala Phe Gly Met Ala Phe Ala Val Val Asp Ala Cys
50 55 60

Pro Lys Tyr Cys Val Cys Gln Asn Leu Ser Glu Ser Leu Gly Thr Leu
65 70 75 80

Cys Pro Ser Lys Gly Leu Leu Phe Val Pro Pro Asp Ile Asp Arg Arg
85 90 95

Thr Val Glu Leu Arg Leu Gly Gly Asn Phe Ile Ile His Ile Ser Arg
100 105 110

Gln Asp Phe Ala Asn Met Thr Gly Leu Val Asp Leu Thr Leu Ser Arg

115					120					125					
Asn	Thr	Ile	Ser	His	Ile	Gln	Pro	Phe	Ser	Phe	Leu	Asp	Leu	Glu	Ser
130					135					140					
Leu	Arg	Ser	Leu	His	Leu	Asp	Ser	Asn	Arg	Leu	Pro	Ser	Leu	Gly	Glu
145					150					155					
Asp	Thr	Leu	Arg	Gly	Leu	Val	Asn	Leu	Gln	His	Leu	Ile	Val	Asn	Asn
165					170					175					
Asn	Gln	Leu	Gly	Gly	Ile	Ala	Asp	Glu	Ala	Phe	Glu	Asp	Phe	Leu	Leu
180					185					190					
Thr	Leu	Glu	Asp	Leu	Asp	Leu	Ser	Tyr	Asn	Asn	Leu	His	Gly	Leu	Pro
195					200					205					
Trp	Asp	Ser	Val	Arg	Arg	Met	Val	Asn	Leu	His	Gln	Leu	Ser	Leu	Asp
210					215					220					
His	Asn	Leu	Leu	Asp	His	Ile	Ala	Glu	Gly	Thr	Phe	Ala	Asp	Leu	Gln
225					230					235					
Lys	Leu	Ala	Arg	Leu	Asp	Leu	Thr	Ser	Asn	Arg	Leu	Gln	Lys	Leu	Pro
245					250					255					
Pro	Asp	Pro	Ile	Phe	Ala	Arg	Ser	Gln	Ala	Ser	Ala	Leu	Thr	Ala	Thr
260					265					270					
Pro	Phe	Ala	Pro	Pro	Leu	Ser	Phe	Ser	Phe	Gly	Gly	Asn	Pro	Leu	His
275					280					285					
Cys	Asn	Cys	Glu	Leu	Leu	Trp	Leu	Arg	Arg	Leu	Glu	Arg	Asp	Asp	Asp
290					295					300					
Leu	Glu	Thr	Cys	Gly	Ser	Pro	Gly	Gly	Leu	Lys	Gly	Arg	Tyr	Phe	Trp
305					310					315					
His	Val	Arg	Glu	Glu	Glu	Phe	Val	Cys	Glu	Pro	Pro	Leu	Ile	Thr	Gln
325					330					335					
His	Thr	His	Lys	Leu	Leu	Val	Leu	Glu	Gly	Gln	Ala	Ala	Thr	Leu	Lys
340					345					350					
Cys	Lys	Ala	Ile	Gly	Asp	Pro	Ser	Pro	Leu	Ile	His	Trp	Val	Ala	Pro
355					360					365					
Asp	Asp	Arg	Leu	Val	Gly	Asn	Ser	Ser	Arg	Thr	Ala	Val	Tyr	Asp	Asn
370					375					380					
Gly	Thr	Leu	Asp	Ile	Phe	Ile	Thr	Thr	Ser	Gln	Asp	Ser	Gly	Ala	Phe
385					390					395					
Thr	Cys	Ile	Ala	Ala	Asn	Ala	Ala	Gly	Glu	Ala	Thr	Ala	Met	Val	Glu
405					410					415					
Val	Ser	Ile	Val	Gln	Leu	Pro	His	Leu	Ser	Asn	Ser	Thr	Ser	Arg	Thr

420					425					430					
Ala	Pro	Pro	Lys	Ser	Arg	Leu	Ser	Asp	Ile	Thr	Gly	Ser	Ser	Lys	Thr
	435					440						445			
Ser	Arg	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Glu	Pro	Pro	Lys	Ser	Pro
	450					455					460				
Pro	Glu	Arg	Ala	Val	Leu	Val	Ser	Glu	Val	Thr	Thr	Thr	Ser	Ala	Leu
	465					470					475				480
Val	Lys	Trp	Ser	Val	Ser	Lys	Ser	Ala	Pro	Arg	Val	Lys	Met	Tyr	Gln
			485						490					495	
Leu	Gln	Tyr	Asn	Cys	Ser	Asp	Asp	Glu	Val	Leu	Ile	Tyr	Arg	Met	Ile
			500					505					510		
Pro	Ala	Ser	Asn	Lys	Ala	Phe	Val	Val	Asn	Asn	Leu	Val	Ser	Gly	Thr
			515				520					525			
Gly	Tyr	Asp	Leu	Cys	Val	Leu	Ala	Met	Trp	Asp	Asp	Thr	Ala	Thr	Thr
	530					535					540				
Leu	Thr	Ala	Thr	Asn	Ile	Val	Gly	Cys	Ala	Gln	Phe	Phe	Thr	Lys	Ala
	545					550					555				560
Asp	Tyr	Pro	Gln	Cys	Gln	Ser	Met	His	Ser	Gln	Ile	Leu	Gly	Gly	Thr
			565						570					575	
Met	Ile	Leu	Val	Ile	Gly	Gly	Ile	Ile	Val	Ala	Thr	Leu	Leu	Val	Phe
			580					585					590		
Ile	Val	Ile	Leu	Met	Val	Arg	Tyr	Lys	Val	Cys	Asn	His	Glu	Ala	Pro
	595						600					605			
Ser	Lys	Met	Ala	Ala	Ala	Val	Ser	Asn	Val	Tyr	Ser	Gln	Thr	Asn	Gly
	610					615					620				
Ala	Gln	Pro	Pro	Pro	Pro	Ser	Ser	Ala	Pro	Ala	Gly	Ala	Pro	Pro	Gln
	625					630					635				640
Gly	Pro	Pro	Lys	Val	Val	Val	Arg	Asn	Glu	Leu	Leu	Asp	Phe	Thr	Ala
			645						650				655		
Ser	Leu	Ala	Arg	Ala	Ser	Asp	Ser	Ser	Ser	Ser	Ser	Ser	Leu	Gly	Ser
			660				665						670		
Gly	Glu	Ala	Ala	Gly	Leu	Gly	Arg	Ala	Pro	Trp	Arg	Ile	Pro	Pro	Ser
	675						680					685			
Ala	Pro	Arg	Pro	Lys	Pro	Ser	Leu	Asp	Arg	Leu	Met	Gly	Ala	Phe	Ala
	690						695					700			
Ser	Leu	Asp	Leu	Lys	Ser	Gln	Arg	Lys	Glu	Glu	Leu	Leu	Asp	Ser	Arg
	705					710					715				720
Thr	Pro	Ala	Gly	Arg	Gly	Ala	Gly	Thr	Ser	Ala	Arg	Gly	His	His	Ser

725					730					735					
Asp	Arg	Glu	Pro	Leu	Leu	Gly	Pro	Pro	Ala	Ala	Arg	Ala	Arg	Ser	Leu
			740					745					750		
Leu	Pro	Leu	Pro	Leu	Glu	Gly	Lys	Ala	Lys	Arg	Ser	His	Ser	Phe	Asp
		755					760					765			
Met	Gly	Asp	Phe	Ala	Ala	Ala	Ala	Ala	Gly	Gly	Val	Val	Pro	Gly	Gly
	770					775					780				
Tyr	Ser	Pro	Pro	Arg	Lys	Val	Ser	Asn	Ile	Trp	Thr	Lys	Arg	Ser	Leu
785						790					795				800
Ser	Val	Asn	Gly	Met	Leu	Leu	Pro	Phe	Glu	Glu	Ser	Asp	Leu	Val	Gly
				805					810					815	
Ala	Arg	Gly	Thr	Phe	Gly	Ser	Ser	Glu	Trp	Val	Met	Glu	Ser	Thr	Val
			820					825					830		

<210> 25

<211> 98

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:IFAbd Domain
13-110

<400> 25

Gln	Phe	Gln	Lys	Glu	Asp	Ala	Ala	Leu	Thr	Ile	Tyr	Glu	Met	Leu	Gln
1				5					10					15	
Asn	Ile	Phe	Ala	Ile	Phe	Arg	Gln	Asp	Ser	Ser	Ser	Thr	Gly	Trp	Asn
			20					25					30		
Glu	Thr	Ile	Val	Glu	Asn	Leu	Leu	Ala	Asn	Val	Tyr	His	Gln	Ile	Asn
			35					40					45		
His	Leu	Lys	Thr	Val	Leu	Glu	Glu	Lys	Leu	Glu	Lys	Glu	Asp	Phe	Thr
	50					55				60					
Arg	Gly	Lys	Leu	Met	Ser	Ser	Leu	His	Leu	Lys	Arg	Tyr	Tyr	Gly	Arg
65					70					75					80
Ile	Leu	His	Tyr	Leu	Lys	Ala	Lys	Glu	Tyr	Ser	His	Cys	Ala	Trp	Thr
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Ile	Val														

<210> 26

<211> 183
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:pfam00143
Domain 5-187

<400> 26
Ser Ser Phe Leu Val Ala Leu Val Ala Leu Gly Cys Asn Ser Val Cys
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Ser Leu Gly Cys Asp Leu Pro Gln Thr His Gly Leu Leu Asn Arg Arg
20 25 30
Ala Leu Thr Leu Leu Gly Gln Met Arg Arg Leu Pro Ala Ser Ser Cys
35 40 45
Gln Lys Asp Arg Asn Asp Phe Ala Phe Pro Gln Asp Val Phe Gly Gly
50 55 60
Asp Gln Ser His Lys Ala Gln Ala Leu Ser Val Val His Val Thr Asn
65 70 75 80
Gln Lys Ile Phe His Phe Phe Cys Thr Glu Ala Ser Ser Ser Ala Ala
85 90 95
Trp Asn Thr Thr Leu Leu Glu Glu Phe Cys Thr Gly Leu Asp Arg Gln
100 105 110
Leu Thr Arg Leu Glu Ala Cys Val Leu Gln Glu Val Glu Glu Gly Glu
115 120 125
Ala Pro Leu Thr Asn Glu Asp Ile His Pro Glu Asp Ser Ile Leu Arg
130 135 140
Asn Tyr Phe Gln Arg Leu Ser Leu Tyr Leu Gln Glu Lys Lys Tyr Ser
145 150 155 160
Pro Cys Ala Trp Glu Ile Val Arg Ala Glu Ile Met Arg Ser Leu Tyr
165 170 175
Tyr Ser Ser Thr Ala Leu Gln
180

See
Cl
cont